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## RAW SEQUENCE LISTING

DATE: 03/22/2002

PATENT APPLICATION: US/09/966,955A

TIME: 14:45:54

Input Set : A:\D029 Sequence Listing.corrected.1.15.01.txt

Output Set: N:\CRF3\03222002\I966955A.raw

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3 <110> APPLICANT: Perez-Villar, Juan J.
4   Chang, Han
5   Yang, Wen-Pin
6   Wu, Yuli
7   Whitney, Gena S.
8   Kanner, Steven B.
10 <120> TITLE OF INVENTION: Identification and Cloning of a Full-length Human
11   Clnk-related Gene, MIST (Mast Cell Immunoreceptor
12   Signal Transducer)
14 <130> FILE REFERENCE: 3053-4113US1
16 <140> CURRENT APPLICATION NUMBER: US/09/966,955A
17 <141> CURRENT FILING DATE: 2001-09-28
19 <150> PRIOR APPLICATION NUMBER: 60/237030
20 <151> PRIOR FILING DATE: 2000-09-29
22 <160> NUMBER OF SEQ ID NOS: 52
24 <170> SOFTWARE: PatentIn Ver. 2.1
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27 <211> LENGTH: 1851
28 <212> TYPE: DNA
29 <213> ORGANISM: HUMAN
31 <220> FEATURE:
32 <223> OTHER INFORMATION: HUMAN FULL-LENGTH MIST cDNA CLONE #8 - NUCLEIC
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38 ccagaggtcc aagatcctta caagggggcc agaaagggat gagctttctg aagaagcact 180
39 gatgtaaaat accaggaatt ttgacatcga agaagatttt tgtgatggca gctgggattt 240
40 ggccataatc tagaagacac atggtgaata cagttgcaag tcatttagtc atatttcttg 300
41 ctaaatgtgt gtgtcttcaa tggctgaatt gaagatccct cttacccgcc aggtgccaag 360
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49 caaggacgtc agaagccaaa acattaaagg agatgcatcc gtaagaaaga acaagattcc 840
50 ttaccacct cctcggcctc tcataacact tccgaagaag taccaaccct tgccccctga 900
51 gccggagagc agcaggccac ctttatctca gagacacacc tttccagaag tccagagaat 960
52 gccagtcag ataagcttaa gggacttaag tgaggtcctt gaagcagaaa aagttcctca 1020
53 taaccagagg aagcctgaat caactcatct gttagaaaac caaataactc aagagattcc 1080
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57 tgatagaaaag gatgtccagc acaatgaatg gtacattgga gaatacagcc gccaggcagt 1320
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62 aattgatggg aaagataaaa ctgggggtcca caggaaacag tgtcacctca ctcagccact 1620
63 ccctctcacc agacacctct tgcctctgta gcctggtctt tgtgttatct ttggtttact 1680
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65 gacaactttt ttaactttgg agaaaaagaaa aacactctat aacagagagt ggaaaaatcac 1800
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74 <220> FEATURE:
75 <223> OTHER INFORMATION: HUMAN FULL-LENGTH MIST cDNA CLONE #8, TRANSLATED
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78 <400> SEQUENCE: 2
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83 20 25 30
85 Lys Phe Gln Asn Phe Ser Leu Pro Lys Asn Arg Ser Trp Pro Arg Ile
86 35 40 45
88 Asn Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu Asp
89 50 55 60
91 Trp Glu Arg Asn Phe Ala Ala Val Leu Asp Gly Ala Lys Gly His Ser
92 65 70 75 80
94 Asp Asp Asp Tyr Asp Asp Pro Glu Leu Arg Met Glu Glu Thr Trp Gln
95 85 90 95
97 Ser Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr Ala
98 100 105 110
100 Asp Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu Asp
101 115 120 125
103 Thr Arg Thr Ser Ile Ser Ile Gly Gln Pro Thr Trp Asn Thr Gln Thr
104 130 135 140
106 Arg Leu Glu Arg Val Asp Lys Pro Ile Ser Lys Asp Val Arg Ser Gln
107 145 150 155 160
109 Asn Ile Lys Gly Asp Ala Ser Val Arg Lys Asn Lys Ile Pro Leu Pro
110 165 170 175
112 Pro Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu Pro
113 180 185 190
115 Pro Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr Phe
116 195 200 205
118 Pro Glu Val Gln Arg Met Pro Ser Gln Ile Ser Leu Arg Asp Leu Ser
119 210 215 220
121 Glu Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro Glu

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125          245          250          255
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128          260          265          270
130 Asp His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln Pro
131          275          280          285
133 Pro Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr Thr
134          290          295          300
136 Ser Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val Gln
137 305          310          315          320
139 His Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu Glu
140          325          330          335
142 Ala Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp Cys
143          340          345          350
145 Ser Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr Glu
146          355          360          365
148 Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln Gln
149          370          375          380
151 Phe Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser Val
152 385          390          395          400
154 Glu Asp Ile Ile Glu His Tyr Lys Asn Phe Pro Ile Ile Leu Ile Asp
155          405          410          415
157 Gly Lys Asp Lys Thr Gly Val His Arg Lys Gln Cys His Leu Thr Gln
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160 Pro Leu Pro Leu Thr Arg His Leu Leu Pro Leu
161          435          440
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166 <212> TYPE: DNA
167 <213> ORGANISM: HUMAN
169 <220> FEATURE:
170 <223> OTHER INFORMATION: HUMAN MIST SPLICE VARIANT cDNA CLONE #7, NUCLEIC
171 ACID SEQUENCE
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175 caggagggttt tctgctgaag ggcactgctt agcatcgaga agaattcaac ccaccgcctt 120
176 actaatttcc agtgccccaâ ggtctctgca ctgcccggcc tcctcacagg agacggacac 180
177 ctccagcctag atcccttggt gctctccacg ctgttcaggc tgaattgaag atccctctta 240
178 cccgccagggt gccâagaact atgaacaggc agggcaatag aaagacaact aaagaaggat 300
179 ccaacgattt gaaattccag aacttcagtc tgccââââââ caggtcatgg cctcgcacat 360
180 atagtgccac aggccagtac cagaggatga acaagcctct tctagactgg gaaagaaact 420
181 ttgctgcagt cctggatgga gcaâââaggcc acagtgatga tgactatgat gaccctgagc 480
182 ttcggatgga agagacatgg cagtcgatta aaattttacc agcccggcct atâââggaat 540
183 ctgaatatgc agatacacac tatttcaagg ttgcaatgga cactcccctt ccgtagaca 600
184 ccaggacctc tatctccatt ggacagccga cctggaacac acagacgagg ttggââââgag 660
185 tggacââââc catttccââg gacgtcagââ gccâââââc taaaggagat gcatccgtaa 720
186 gââââââââ gattccttta ccacctcctc ggccctctcat aacacttccg aagaagtacc 780
187 aacccttgcc ccctgagccg gagagcagca ggccaccttt atctcagaga cacacctttc 840

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190 atactcaaga gattccaactt gccattagca gttcttcatt cacgacaagc aaccacagtg 1020
191 tgcaaaacag agatcataga ggaggcatgc agccctgttc tcctcagaga tgccagcctc 1080
192 cagccagctg cagccctcac gaaaatatac tgccctataa atacacaagc tggagaccac 1140
193 ctttccccc aaaggtctgat agaaaggatg tccagcaca tgaatggtac attggagaat 1200
194 acagccgcca ggcagtggaa gaggcattca tgaaggagaa caaggatggt agtttcttgg 1260
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197 caggactcag aggagatgag aagtttgatt cagtagaaga catcatcgaa cactacaaga 1440
198 attttcccat tatactaatt gatgggaaa ataaaaactgg ggtccacagg aaacagtgtc 1500
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202 gagagtggaa aatcactcac ggttttgaaa gttcaaacca cagagaaaat atttataaca 1740
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205 gctcatgata caggcgagca gcaaagggca ccagaagctg ttgcttaa at gtttgagctc 1920
206 agtgcaagac aagtctatgg gaaattccca aatctgtgct ctttacagga cactgcgctg 1980
207 cctttatgtc agttgttggg ccttacatat atacaatgtg tggatgattt cttacactaa 2040
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211 tcgggagggt gaggcaggag aatggtgtga acccgggagg cggagcttgc agtgagccga 2280
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215 &lt;210&gt; SEQ ID NO: 4

216 &lt;211&gt; LENGTH: 428

217 &lt;212&gt; TYPE: PRT

218 &lt;213&gt; ORGANISM: HUMAN

220 &lt;220&gt; FEATURE:

221 <223> OTHER INFORMATION: HUMAN MIST SPLICE VARIANT CLONE #7, AMINO ACID  
 222 SEQUENCE

224 &lt;400&gt; SEQUENCE: 4

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229           20           25           30
231 Ile Asn Ser Ala Thr Gly Gln Tyr Gln Arg Met Asn Lys Pro Leu Leu
232       35       40       45
234 Asp Trp Glu Arg Asn Phe Ala Val Leu Asp Gly Ala Lys Gly His
235   50       55       60
237 Ser Asp Asp Asp Tyr Asp Pro Glu Leu Arg Met Glu Glu Thr Trp
238   65       70       75       80
240 Gln Ser Ile Lys Ile Leu Pro Ala Arg Pro Ile Lys Glu Ser Glu Tyr
241           85           90           95
243 Ala Asp Thr His Tyr Phe Lys Val Ala Met Asp Thr Pro Leu Pro Leu
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255 Pro Pro Pro Arg Pro Leu Ile Thr Leu Pro Lys Lys Tyr Gln Pro Leu
256      165      170      175
258 Pro Pro Glu Pro Glu Ser Ser Arg Pro Pro Leu Ser Gln Arg His Thr
259      180      185      190
261 Phe Pro Glu Val Gln Arg Met Pro Ser Gln Ile Ser Leu Arg Asp Leu
262      195      200      205
264 Ser Glu Val Leu Glu Ala Glu Lys Val Pro His Asn Gln Arg Lys Pro
265      210      215      220
267 Glu Ser Thr His Leu Leu Glu Asn Gln Asn Thr Gln Glu Ile Pro Leu
268 225      230      235      240
270 Ala Ile Ser Ser Ser Ser Phe Thr Thr Ser Asn His Ser Val Gln Asn
271      245      250      255
273 Arg Asp His Arg Gly Gly Met Gln Pro Cys Ser Pro Gln Arg Cys Gln
274      260      265      270
276 Pro Pro Ala Ser Cys Ser Pro His Glu Asn Ile Leu Pro Tyr Lys Tyr
277      275      280      285
279 Thr Ser Trp Arg Pro Pro Phe Pro Lys Arg Ser Asp Arg Lys Asp Val
280      290      295      300
282 Gln His Asn Glu Trp Tyr Ile Gly Glu Tyr Ser Arg Gln Ala Val Glu
283 305      310      315      320
285 Glu Ala Phe Met Lys Glu Asn Lys Asp Gly Ser Phe Leu Val Arg Asp
286      325      330      335
288 Cys Ser Thr Lys Ser Lys Glu Glu Pro Tyr Val Leu Ala Val Phe Tyr
289      340      345      350
291 Glu Asn Lys Val Tyr Asn Val Lys Ile Arg Phe Leu Glu Arg Asn Gln
292      355      360      365
294 Gln Phe Ala Leu Gly Thr Gly Leu Arg Gly Asp Glu Lys Phe Asp Ser
295      370      375      380
297 Val Glu Asp Ile Ile Glu His Tyr Lys Asn Phe Pro Ile Ile Leu Ile
298 385      390      395      400
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**VERIFICATION SUMMARY**

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